

SEQUENCE LISTING

<110> Merck Patent GmbH

5 <120> Novelacute neuronal induced Calcium binding protein

<130> ANICBP2IDWS

<140>

10 <141>

<160> 2

15 <170> PatentIn Ver. 2.1

<210> 1

<211> 1014

<212> DNA

20 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1014)

25 <400> 1

atg	aaa	aaa	atg	cct	ttg	ttt	agt	aaa	tca	cac	aaa	aat	cca	gca	gaa	48
Met	Lys	Lys	Met	Pro	Leu	Phe	Ser	Lys	Ser	His	Lys	Asn	Pro	Ala	Glu	
1				5					10					15		
att	gtg	aaa	atc	ctg	aaa	gac	aat	ttg	gcc	att	ttg	gaa	aag	caa	gac	96
Ile	Val	Lys	Ile	Leu	Lys	Asp	Asn	Leu	Ala	Ile	Leu	Glu	Lys	Gln	Asp	
			20					25					30			
aaa	aag	aca	gac	aag	gct	tca	gaa	gaa	gtg	tct	aaa	tca	ctg	caa	gca	144
Lys	Lys	Thr	Asp	Lys	Ala	Ser	Glu	Glu	Val	Ser	Lys	Ser	Leu	Gln	Ala	
		35					40					45				
atg	aaa	gaa	att	ctg	tgt	ggc	aca	aac	gag	aaa	gaa	ccc	cca	aca	gaa	192
Met	Lys	Glu	Ile	Leu	Cys	Gly	Thr	Asn	Glu	Lys	Glu	Pro	Pro	Thr	Glu	
	50					55					60					
gca	gtg	gct	cag	cta	gca	caa	gaa	ctc	tac	agc	agt	ggc	ctg	cta	gtg	240
Ala	Val	Ala	Gln	Leu	Ala	Gln	Glu	Leu	Tyr	Ser	Ser	Gly	Leu	Leu	Val	
45	65				70				75					80		
aca	ctg	ata	gct	gac	ctg	cag	ctg	ata	gac	ttt	gag	gga	aaa	aaa	gat	288
Thr	Leu	Ile	Ala	Asp	Leu	Gln	Leu	Ile	Asp	Phe	Glu	Gly	Lys	Lys	Asp	
			85					90						95		
gtg	acc	cag	ata	ttt	aac	aac	atc	ttg	aga	aga	cag	ata	ggc	act	cgg	336
Val	Thr	Gln	Ile	Phe	Asn	Asn	Ile	Leu	Arg	Arg	Gln	Ile	Gly	Thr	Arg	
			100					105					110			
agt	cct	act	gtg	gag	tat	att	agt	gct	cat	cct	cat	atc	ctg	ttt	atg	384
Ser	Pro	Thr	Val	Glu	Tyr	Ile	Ser	Ala	His	Pro	His	Ile	Leu	Phe	Met	
		115					120					125				
ctc	ctc	aaa	gga	tat	gaa	gcc	cca	cag	att	gcc	tta	cgt	tgt	ggg	att	432
Leu	Leu	Lys	Gly	Tyr	Glu	Ala	Pro	Gln	Ile	Ala	Leu	Arg	Cys	Gly	Ile	
	130					135					140					

	atg ctg aga gaa tgt att cga cat gaa cca ctt gcc aaa atc atc ctc	480
	Met Leu Arg Glu Cys Ile Arg His Glu Pro Leu Ala Lys Ile Ile Leu	
	145 150 155 160	
5	ttt tct aat caa ttc aga gat ttc ttt aag tac gtg gag ttg tca aca	528
	Phe Ser Asn Gln Phe Arg Asp Phe Phe Lys Tyr Val Glu Leu Ser Thr	
	165 170 175	
10	ttt gat att gct tca gat gcc ttt gct act ttc aag gat tta cta acc	576
	Phe Asp Ile Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu Thr	
	180 185 190	
15	aga cat aaa gtg ttg gta gca gac ttc tta gaa caa aat tac gac act	624
	Arg His Lys Val Leu Val Ala Asp Phe Leu Glu Gln Asn Tyr Asp Thr	
	195 200 205	
20	att ttt gaa gac tat gag aaa ttg ctt cag tct gag aat tat gtt act	672
	Ile Phe Glu Asp Tyr Glu Lys Leu Leu Gln Ser Glu Asn Tyr Val Thr	
	210 215 220	
25	aag aga cag tct tta aag ctg cta ggg gag ctg atc ctg gac cgt cac	720
	Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Ile Leu Asp Arg His	
	225 230 235 240	
30	aac ttt gcc atc atg aca aag tat atc agc aag ccg gag aac ctg aaa	768
	Asn Phe Ala Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu Lys	
	245 250 255	
35	ctc atg atg aac ctc ctt cgg gat aaa agt ccc aac atc cag ttt gaa	816
	Leu Met Met Asn Leu Leu Arg Asp Lys Ser Pro Asn Ile Gln Phe Glu	
	260 265 270	
40	gcc ttt cat gtt ttt aag gtg ttt gtg gcc agt cct cac aaa aca cag	864
	Ala Phe His Val Phe Lys Val Phe Val Ala Ser Pro His Lys Thr Gln	
	275 280 285	
45	cct att gtg gag atc ctg tta aaa aat cag ccc aaa ctc att gag ttt	912
	Pro Ile Val Glu Ile Leu Leu Lys Asn Gln Pro Lys Leu Ile Glu Phe	
	290 295 300	
50	ctg agc agc ttc caa aaa gaa agg acg gat gat gag cag ttc gct gac	960
	Leu Ser Ser Phe Gln Lys Glu Arg Thr Asp Asp Glu Gln Phe Ala Asp	
	305 310 315 320	
55	gag aag aac tac ttg att aaa cag atc cga gac ttg aag aaa acg gcc	1008
	Glu Lys Asn Tyr Leu Ile Lys Gln Ile Arg Asp Leu Lys Lys Thr Ala	
	325 330 335	
60	cct tga	1014
	Pro	
	<210> 2	
	<211> 337	
	<212> PRT	
	<213> Homo sapiens	
	<400> 2	
	Met Lys Lys Met Pro Leu Phe Ser Lys Ser His Lys Asn Pro Ala Glu	
	1 5 10 15	

	Ile	Val	Lys	Ile	Leu	Lys	Asp	Asn	Leu	Ala	Ile	Leu	Glu	Lys	Gln	Asp
				20					25					30		
	Lys	Lys	Thr	Asp	Lys	Ala	Ser	Glu	Glu	Val	Ser	Lys	Ser	Leu	Gln	Ala
			35					40					45			
5	Met	Lys	Glu	Ile	Leu	Cys	Gly	Thr	Asn	Glu	Lys	Glu	Pro	Pro	Thr	Glu
	50						55					60				
	Ala	Val	Ala	Gln	Leu	Ala	Gln	Glu	Leu	Tyr	Ser	Ser	Gly	Leu	Leu	Val
	65					70					75					80
	Thr	Leu	Ile	Ala	Asp	Leu	Gln	Leu	Ile	Asp	Phe	Glu	Gly	Lys	Lys	Asp
10					85					90					95	
	Val	Thr	Gln	Ile	Phe	Asn	Asn	Ile	Leu	Arg	Arg	Gln	Ile	Gly	Thr	Arg
				100					105					110		
	Ser	Pro	Thr	Val	Glu	Tyr	Ile	Ser	Ala	His	Pro	His	Ile	Leu	Phe	Met
			115					120					125			
15	Leu	Leu	Lys	Gly	Tyr	Glu	Ala	Pro	Gln	Ile	Ala	Leu	Arg	Cys	Gly	Ile
	130						135					140				
	Met	Leu	Arg	Glu	Cys	Ile	Arg	His	Glu	Pro	Leu	Ala	Lys	Ile	Ile	Leu
	145					150					155					160
	Phe	Ser	Asn	Gln	Phe	Arg	Asp	Phe	Phe	Lys	Tyr	Val	Glu	Leu	Ser	Thr
20					165					170					175	
	Phe	Asp	Ile	Ala	Ser	Asp	Ala	Phe	Ala	Thr	Phe	Lys	Asp	Leu	Leu	Thr
				180					185					190		
	Arg	His	Lys	Val	Leu	Val	Ala	Asp	Phe	Leu	Glu	Gln	Asn	Tyr	Asp	Thr
			195					200					205			
25	Ile	Phe	Glu	Asp	Tyr	Glu	Lys	Leu	Leu	Gln	Ser	Glu	Asn	Tyr	Val	Thr
	210						215					220				
	Lys	Arg	Gln	Ser	Leu	Lys	Leu	Leu	Gly	Glu	Leu	Ile	Leu	Asp	Arg	His
	225					230					235					240
	Asn	Phe	Ala	Ile	Met	Thr	Lys	Tyr	Ile	Ser	Lys	Pro	Glu	Asn	Leu	Lys
30					245					250					255	
	Leu	Met	Met	Asn	Leu	Leu	Arg	Asp	Lys	Ser	Pro	Asn	Ile	Gln	Phe	Glu
				260					265					270		
	Ala	Phe	His	Val	Phe	Lys	Val	Phe	Val	Ala	Ser	Pro	His	Lys	Thr	Gln
			275					280					285			
35	Pro	Ile	Val	Glu	Ile	Leu	Leu	Lys	Asn	Gln	Pro	Lys	Leu	Ile	Glu	Phe
	290						295					300				
	Leu	Ser	Ser	Phe	Gln	Lys	Glu	Arg	Thr	Asp	Asp	Glu	Gln	Phe	Ala	Asp
	305					310					315					320
	Glu	Lys	Asn	Tyr	Leu	Ile	Lys	Gln	Ile	Arg	Asp	Leu	Lys	Lys	Thr	Ala
40					325					330					335	
	Pro															